RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/677,956A
Source: IFW16
Date Processed by STIC: 07/07/2006

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 07/07/2006
PATENT APPLICATION: US/10/677,956A TIME: 17:08:11

Input Set : A:\323-100USD.ST25.txt
Output Set: N:\CRF4\07072006\J677956A.raw

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 5 <110> APPLICANT: Zebedee, Suzanne
 6       Inchauspe, Genevieve
 7       Nasoff, Marc S.
 8       Prince, Alfred M.
10 <120> TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT VIRAL ANTIGENS
12 <130> FILE REFERENCE: 323-100USD
14 <140> CURRENT APPLICATION NUMBER: 10/677,956A
15 <141> CURRENT FILING DATE: 2003-10-01
17 <150> PRIOR APPLICATION NUMBER: 08/931,855
18 <151> PRIOR FILING DATE: 1997-09-16
20 <150> PRIOR APPLICATION NUMBER: 08/563,733
21 <151> PRIOR FILING DATE: 1995-11-08
23 <150> PRIOR APPLICATION NUMBER: 08/272,271
24 <151> PRIOR FILING DATE: 1994-07-08
26 <150> PRIOR APPLICATION NUMBER: 07/616,369
27 <151> PRIOR FILING DATE: 1990-11-21
29 <150> PRIOR APPLICATION NUMBER: 07/573,643
30 <151> PRIOR FILING DATE: 1990-08-27
32 <160> NUMBER OF SEQ ID NOS: 71
34 <170> SOFTWARE: PatentIn version 3.3
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 795
38 <212> TYPE: DNA
39 <213> ORGANISM: Human immunodeficiency virus
42 <220> FEATURE:
43 <221> NAME/KEY: CDS
44 <222> LOCATION: (16)..(789)
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49                  1               5                   10
51 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
52 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
53         15                  20                  25
55 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta     147
56 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
57     30                  35                  40
59 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg     195
60 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
61 45                  50                  55                  60
63 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag     243
64 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
65                 65                  70                  75
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68 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
69             80                  85                  90
71 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act      339
72 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
73         95                  100                 105
75 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
76 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
77     110                 115                 120
79 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
80 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
81 125                 130                 135                 140
83 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
84 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
85                 145                 150                 155
87 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
88 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
89             160                 165                 170
91 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
92 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
93         175                 180                 185
95 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
96 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
97     190                 195                 200
99 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
100 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
101 205                 210                 215                 220
103 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt      723
104 Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys
105                 225                 230                 235
107 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc      771
108 Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
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119 <213> ORGANISM: Human immunodeficiency virus
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128             20                  25                  30
131 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
132         35                  40                  45
135 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
136     50                  55                  60
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144                 85                  90                  95
147 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
148             100                 105                 110
151 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
152         115                 120                 125
155 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
156     130                 135                 140
159 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
160 145                 150                 155                 160
163 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
164                 165                 170                 175
167 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
168             180                 185                 190
171 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
172         195                 200                 205
175 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
176     210                 215                 220
179 Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu
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184                 245                 250                 255
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193 <212> TYPE: DNA
194 <213> ORGANISM: Human immunodeficiency virus
197 <220> FEATURE:
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199 <222> LOCATION: (16)..(789)
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204                  1               5                  10
206 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
207 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
208         15                  20                  25
210 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta     147
211 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
212     30                  35                  40
214 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg     195
215 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
216 45                  50                  55                  60
218 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag     243
219 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
220                 65                  70                  75
222 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att     291
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Input Set : A:\323-100USD.ST25.txt
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223 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
224             80                  85                  90
226 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act      339
227 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
228         95                  100                 105
230 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
231 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
232     110                 115                 120
234 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
235 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
236 125                 130                 135                 140
238 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
239 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
240                 145                 150                 155
242 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
243 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
244             160                 165                 170
246 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
247 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
248         175                 180                 185
250 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
251 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
252     190                 195                 200
254 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
255 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
256 205                 210                 215                 220
258 gga gta gga gga ccc aaa aat caa caa aga tta aat tta tgg ggg tgt      723
259 Gly Val Gly Gly Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys
260                 225                 230                 235
262 aaa ggg aaa ctt att tgt tat act tcc gtt aaa tgg aat gga ccc ggc      771
263 Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
264             240                 245                 250
266 cat aag gca aga gtt ttg taataa                                     795
267 His Lys Ala Arg Val Leu
268         255
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272 <211> LENGTH: 258
273 <212> TYPE: PRT
274 <213> ORGANISM: Human immunodeficiency virus
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283             20                  25                  30
286 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
287         35                  40                  45
290 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
291     50                  55                  60
294 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
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Input Set : A:\323-100USD.ST25.txt
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298 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
299                 85                  90                  95
302 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
303             100                 105                 110
306 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
307         115                 120                 125
310 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
311     130                 135                 140
314 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
315 145                 150                 155                 160
318 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
319                 165                 170                 175
322 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
323             180                 185                 190
326 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
327         195                 200                 205
330 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
331     210                 215                 220
334 Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu
335 225                 230                 235                 240
338 Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg
339                 245                 250                 255
342 Val Leu
346 <210> SEQ ID NO: 5
347 <211> LENGTH: 795
348 <212> TYPE: DNA
349 <213> ORGANISM: Human immunodeficiency virus
352 <220> FEATURE:
353 <221> NAME/KEY: CDS
354 <222> LOCATION: (16)..(789)
356 <400> SEQUENCE: 5
357 aggagggttt ttcat atg cca atc gtg cag aac atc cag ggg caa atg gta      51
358                  Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
359                  1               5                  10
361 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
362 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
363         15                  20                  25
365 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta     147
366 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
367     30                  35                  40
369 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg     195
370 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
371 45                  50                  55                  60
373 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag     243
374 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
375                 65                  70                  75
377 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att     291
378 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/07/2006
PATENT APPLICATION: US/10/677,956A TIME: 17:08:12

Input Set : A:\323-100USD.ST25.txt
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:19,20,21,22,23,24,25,26,27,28,29,31,32,33,34,35,36,37,38,39,40,41,42,43
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Seq#:68,69,70,71

VERIFICATION SUMMARY DATE: 07/07/2006
PATENT APPLICATION: US/10/677,956A TIME: 17:08:12

Input Set : A:\323-100USD.ST25.txt
Output Set: N:\CRF4\07072006\J677956A.raw